

1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: Rotkreuzstiftung Zentrallaboratorium
Blutspendedienst
 - (B) STREET: Wankdorfstrasse 10
 - (C) CITY: Bern 22
 - (E) COUNTRY: Switzerland
 - (F) POSTAL CODE (ZIP): CH-3000
- (ii) TITLE OF INVENTION: Recombinant Fab-fragment with reactivity
against Rhesus D antigens, DNA encoding them, complete
antibodies comprising the Fab fragments and process for
their preparation
- (iii) NUMBER OF SEQUENCES: 64
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (v) CURRENT APPLICATION DATA:
 - APPLICATION NUMBER: PCT/EP97/03253
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: EP 96810421.6
 - (B) FILING DATE: 24-JUN-1996

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: Adult
 - (E) HAPLOTYPE: Diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA Library, LD1
 - (B) CLONE: LD1-40
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: Chromosome 14
 - (B) MAP POSITION: q32.3
 - (C) UNITS: Chromosome band number

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3

(B) LOCATION:join(91..105, 148..198, 295..342)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..375

(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG	48
Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	
ACC CTG AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT	96
Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr	
20 25 30	
ACC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG	144
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
ACA GGT ATA TGG TTT GAT GGA AGT AAC AAA AAC TAT GCA GAC TCC GTG	192
Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val	
50 55 60	
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
CTG CAA CTG AAC AGC CTG AGA GAC GAG GAC ACG GCT GTG TAT TAT TGT	288
Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
GCG AGA GAG CGA GCA GCA CGT GGT ATT TCT AGG TTC TAT TAC TAC ATG	336
Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met	
100 105 110	
GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC CCA	375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro	
115 120 125	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr	
20 25 30	
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

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la Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
 50      55      60

/s Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
55      70      75      80

au Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
      85      90      95

la Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met
      100      105      110

sp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro
      115      120      125

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2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: Adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD1
 - (B) CLONE: LD1-40
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: Chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: Chromosome band number
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..318
 - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
- (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(64..96, 142..162, 259..288)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGC GAC AGA
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1              5              10              15

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4

ATC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn	
20 25 30	
GGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG TTG CTG ATC TAT GGT	144
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly	
35 40 45	
TCG TCC ACT TTG CAA AGT GGC GTC CCA TCA AGG TTC AGT GGC AGT GGC	192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
TCT GGG GCA GTT TTC ACT CTC ACC ATC GCC AGT CTA CAA CCT GAA GAT	240
Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp	
65 70 75 80	
TTT GCA ACT TAC TAC TGT CAA GAG AGT TAC AGT AAT CCT CTA ATC ACC	288
Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr	
85 90 95	
ATC GGC CAA GGG ACA CGA CTG GAG ACT AAA	318
Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn	
20 25 30	
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly	
35 40 45	
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp	
65 70 75 80	
Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr	
85 90 95	
Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: Adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA library, LD1
 - (B) CLONE: LD1-52
- (viii) POSITION IN GENOME:
- (A) CHROMOSOME/SEGMENT: Chromosome 14
 - (B) MAP POSITION: q32.3
 - (C) UNITS: Chromosome band number
- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..375
 - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
- (ix) FEATURE:
- (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG	48
Aln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly	
1 5 10 15	
TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC GCC CTC AGA AGT TCT	96
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser	
20 25 30	
AGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG	192
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val	
50 55 60	
AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT	288
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG	336
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met	
100 105 110	

AAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Pln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: Diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA Library, LD1
(B) CLONE: LD1-52

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: Chromosome 2
(B) MAP POSITION: P 11
(C) UNITS: chromosome b.No

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION:1..318
(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3
(B) LOCATION:join(64..96, 142..162, 259..288)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTA	GGA	GAC	AGA	48	
Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5				10						15		
ATC	ACT	TGC	CGG	GCA	AGT	CAG	AAC	ATT	ATC	CGC	TAT	TTA	AAT		96	
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Ile	Arg	Tyr	Leu	Asn	
		20						25					30			
TAT	CAG	CAG	AAG	CCA	GGG	AAA	GCC	CCT	AGG	CTC	CTG	ATC	TAT	GGT	144	
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Arg	Leu	Ile	Tyr	Gly		
		35					40				45					
TCC	ACT	TTG	CAA	AGT	GGG	GTC	CCA	TCA	AGG	TTC	AGT	GGC	AGT	GGA	192	
Ala	Ser	Thr	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	
		50				55					60					
GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGT	AGT	CTG	CAA	CCT	GAA	GAT	240	
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
					70					75				80		
TTT	GCA	ACT	TAC	TAC	TGT	CAA	CAG	AGT	TAC	CGT	ACC	CCT	CCA	TTC	ACT	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Arg	Thr	Pro	Pro	Phe	Thr	
				85					90					95		
TTC	GGC	CCT	GGG	ACC	AAA	GTG	GAG	ATC	AAA						318	
Phe	Gly	Pro	Gly	Thr	Lys	Val	Glu	Ile	Lys							
			100					105								

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg
1				5				10						15	
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Ile	Arg	Tyr	Leu	Asn
			20					25					30		

rp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly
 35 40 45

la Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

er Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

he Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr
 85 90 95

he Gly Pro Gly Thr Lys Val Glu Ile Lys
 100 105

2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: Adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA LIBRARY, LD1
 - (B) CLONE: LD1-84
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: Chromosome 14
 - (B) MAP POSITION: q32.3
 - (C) UNITS: Chromosome band number
- (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(91..105, 148..198, 295..342)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..375
 - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

CC	CTG	AGA	CTC	TCC	TGT	GAA	GCG	TCT	GGA	TTC	ACC	CTC	AGA	AGT	TCT	96
er	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Ser	Ser	
			20					25					30			
GC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCT	GGC	AAG	GGG	CTG	GAG	TGG	GTG	144
ly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
CA	CTT	ATA	TGG	TTT	GAT	GGA	AGT	ATC	AGA	TCG	TAT	GCA	GAA	TCC	GTG	192
la	Leu	Ile	Trp	Phe	Asp	Gly	Ser	Ile	Arg	Ser	Tyr	Ala	Glu	Ser	Val	
	50					55					60					
AG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	ACT	TCC	AAG	AAC	ACC	CTA	TAT	240
ys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Thr	Leu	Tyr	
	65				70					75					80	
TC	CAA	ATG	CGC	AGT	CTG	AGT	GCC	GAC	GAC	ACG	GCT	GTG	TAT	TAC	TGT	288
eu	Gln	Met	Arg	Ser	Leu	Ser	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
CG	AGA	GAC	AAG	GCG	GTT	CGG	GGA	ATT	AGC	AGG	TAC	AAC	TAT	TAC	ATG	336
la	Arg	Asp	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	
			100					105					110			
AC	GTC	TGG	GGC	AAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA				375
asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
		115					120					125				

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5					10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Ser	Ser	
			20					25					30			
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
Ala	Leu	Ile	Trp	Phe	Asp	Gly	Ser	Ile	Arg	Ser	Tyr	Ala	Glu	Ser	Val	
	50					55					60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Thr	Leu	Tyr	
	65				70					75					80	
Leu	Gln	Met	Arg	Ser	Leu	Ser	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90						95		
Ala	Arg	Asp	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	
		100						105					110			
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
		115					120					125				

(2) INFORMATION FOR SEQ ID NO: 11:

- 10
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmune rhsus D donor
 - (D) DEVELOPMENTAL STAGE: Adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA LIBRARY, LD1
 - (B) CLONE: LD1-84
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: Chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: Chromosome band number
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..315
 - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
 - (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	ATA	GGA	GAC	AGA		48
Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Ile	Gly	Asp	Arg		
1				5				10						15			
GTC	ACC	ATC	ACC	TGC	CGG	GCA	AGT	CAG	AGT	ATC	ATC	AGG	TAT	TTG	AAT		96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ile	Arg	Tyr	Leu	Asn		
			20					25					30				
TGG	TAT	CAG	CAC	AAA	CCA	GGA	AAA	GCC	CCT	AAA	CTC	CTC	ATC	TTT	GCT		144
Trp	Tyr	Gln	His	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Phe	Ala		
		35					40					45					
GCA	TCG	AAT	TTG	CAA	ACT	GGG	GTC	CCA	TCC	AGG	TTC	AGT	GGC	AGT	GGA		192
Ala	Ser	Asn	Leu	Gln	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly		
		50				55					60						
TCT	GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGT	GAC	CTG	CAG	CCT	GAG	GAT		240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Asp	Leu	Gln	Pro	Glu	Asp		
65					70				75					80			
TTC	GCA	ACT	TAC	TAC	TGT	CAA	CAG	AGT	TAC	AGT	AGG	CCG	TTC	ACT	TTT		288

he Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe
85 90 95

GC CGG GGG ACC AGC CTG GAC ATC AAA
ly Arg Gly Thr Ser Leu Asp Ile Lys
100 105

315

2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
1 5 10 15
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
20 25 30
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala
35 40 45
Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp
65 70 75 80
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe
85 90 95
Gly Arg Gly Thr Ser Leu Asp Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD1

(B) CLONE: LD1-110

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: Chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..348)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CAG	GTG	AAA	CTG	CTC	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCT	GGG	AGG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1				5					10					15		
TCC	CTG	AGA	CTC	TCC	TGT	ATA	GCG	TCT	GGA	TTC	ACC	CTC	AGG	AAT	TAT	96
Ser	Leu	Arg	Leu	Ser	Cys	Ile	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Asn	Tyr	
			20					25					30			
GCC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG	144
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
GCA	GGT	ATA	TGG	TTT	GAT	GGA	AGC	AAC	AAA	AAC	TAT	GCA	GAC	TCC	GTG	192
Ala	Gly	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Asn	Tyr	Ala	Asp	Ser	Val	
	50					55					60					
AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAC	TCC	AAG	AAC	ACT	CTG	TTT	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe	
	65				70					75				80		
CTG	CAC	ATG	AAC	AGC	CTG	AGA	GCC	GAG	GAC	ACG	GCT	ACA	TAT	TAC	TGT	288
Leu	His	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	
			85						90					95		
GCG	AGA	GAG	AGG	GCG	ATT	CGG	GGA	ATC	AGT	AGA	TAC	AAT	TAC	TAC	ATG	336
Ala	Arg	Glu	Arg	Ala	Ile	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	
			100					105					110			
GAC	GTC	TGG	GGC	AAG	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA				375
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
		115					120					125				

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5					10					15	

Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 65 70 75 80
 Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: Adult
- (E) HAPLOTYPE: Diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA Library, LD1
- (B) CLONE: LD1-110

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: Chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: chromosome b.No

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GTG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTA	GGA	GAC	AGA	48
Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5				10						15		
GTG	ACC	ATC	ACT	TGC	CGG	GCA	AGT	CAG	AGC	ATT	CGA	AGC	TCT	TTA	AAT	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Arg	Ser	Ser	Leu	Asn	
			20					25					30			
TGG	TAT	CAG	CAG	AAA	CCA	GGG	AAA	GCC	CCT	AAA	GTC	CTG	ATC	TAT	GCT	144
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Val	Leu	Ile	Tyr	Ala	
		35					40					45				
GCA	TCC	AGT	TTG	CAA	AGT	GGG	GTC	CCA	TCC	AGG	TTC	AGT	GGC	AGA	GGA	192
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Arg	Gly	
	50					55					60					
TCT	GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGT	CTG	CAG	CCT	GAA	GAT	240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
65					70					75					80	
TTT	GCG	ACT	TAT	TAT	TGT	CAA	CAG	AGT	TCC	AGT	TCC	TCG	TGG	ACG	TTC	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Ser	Ser	Ser	Ser	Trp	Thr	Phe	
				85					90					95		
GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA								315
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys								
			100					105								

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5				10						15		
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Arg	Ser	Ser	Leu	Asn	
			20					25					30			
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Val	Leu	Ile	Tyr	Ala	
		35					40					45				
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Arg	Gly	
	50					55					60					
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
65					70					75					80	
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Ser	Ser	Ser	Ser	Trp	Thr	Phe	
				85					90					95		
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys								
			100					105								

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 (D) DEVELOPMENTAL STAGE: adult
 (E) HAPLOTYPE: diploid
 (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA LIBRARY, LD1
 (B) CLONE: LD1-117
- (viii) POSITION IN GENOME:
 (A) CHROMOSOME/SEGMENT: Chromosome 14
 (B) MAP POSITION: q32.3
 (C) UNITS: Chromosome band number
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..378
 (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
- (ix) FEATURE:
 (A) NAME/KEY: CDR1, CDR2, CDR3
 (B) LOCATION: join(91..105, 148..198, 295..345)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CAG GTG AAA CTG CTC GAG TCA GGA GGA GGC GTG GTC CAG CCT GGG AAG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys	
1 5 10 15	
TCC CTG AGA CTT TCC TGT GCA GCG TCT GGA TTC AGT TTC AAT AGC CAT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His	
20 25 30	
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
GCA TTT ATA TGG TTT GAT GGC AGT AAT AAA TAC TAT GCA GAC TCC GTG	192
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	
50 55 60	
AAG GGC CGA TTC ACC ATC ACC AGA GAC AAC TCC AAG AAC ACG CTG TAT	240
Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC ACG GCT GTC TAT TAC TGT	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	

CGG AGA GAG ACC TCA GTA AGG CTA GGG TAT AGC CGC TAC AAT TAC TAC 336
 Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr
 100 105 110
 ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC ATC TCG TCA 378
 Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr
 100 105 110
 Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor

- (D) DEVELOPMENTAL STAGE: adult
(E) HAPLOTYPE: diploid
(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD1
(B) CLONE: LD1-117

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: Chromosome 2
(B) MAP POSITION: p11
(C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION:1..318
(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
(B) LOCATION:join(64..96, 142..162, 259..288)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GTG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTA	GGA	GAC	AGA	48
Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5				10						15		
GTC	ACC	ATC	ACT	TGC	CGG	GCA	AGT	CAG	AGC	ATT	AGG	AGC	CAT	TTG	AAT	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Arg	Ser	His	Leu	Asn	
			20					25					30			
TGG	TAT	CAG	CAG	AAA	CCA	GGG	AAA	GCC	CCT	AAG	CTC	CTG	ATC	TAT	GCT	144
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				
GCA	TCC	AGT	TTG	CAA	GGT	GGG	GTC	CCA	TCA	AGG	TTC	AGT	GGC	AGT	GGA	192
Ala	Ser	Ser	Leu	Gln	Gly	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	
	50					55					60					
TCT	GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGT	CTG	CAA	CCT	GAA	GAT	240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
65					70				75					80		
TTT	GCA	ACT	TAT	TAC	TGT	CAA	CAG	AGT	TAC	AGG	GCC	CCT	CAG	TGG	ACG	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Arg	Ala	Pro	Gln	Trp	Thr	
			85					90						95		
TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA							318
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys							
		100						105								

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

18

Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg
1				5					10					15	
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Arg	Ser	His	Leu	Asn
			20					25					30		
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala
		35					40					45			
Ala	Ser	Ser	Leu	Gln	Gly	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly
	50					55					60				
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp
65					70					75					80
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Arg	Ala	Pro	Gln	Trp	Thr
				85					90					95	
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys						
			100					105							

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS
- (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
(C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
(E) HAPLOTYPE: diploid
(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA LIBRARY, LD2
(B) CLONE: LD2-1

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
(B) MAP POSITION: q32.3
(C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION:1..375
(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
(B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

00

CAG	GTG	AAA	CTG	CTC	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCG	GGG	GGG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5					10					15		
PCC	CTG	AGA	CTC	TCC	TGT	GTA	GCG	TCT	GGA	TTC	ACC	CTC	AGG	AGT	TAT	96
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Ser	Tyr	
			20					25					30			
GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGC	CTG	GAG	TGG	GTG	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
GCT	TTT	ATA	TGG	TTT	GAT	GGA	AGT	AAT	AAA	GGA	TAT	GTA	GAC	TCC	GTG	192
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val	
	50					55					60					
AAG	GGC	CGA	TTC	ACC	ATC	TCC	CGA	GAC	AAT	TCC	AAG	AAC	ATG	GTC	TAT	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Met	Val	Tyr	
	65				70					75					80	
CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCC	GAT	GAC	ACG	GCT	GTA	TAT	TAT	TGT	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
GCG	AGA	GAG	AAG	GCG	CTT	CGG	GGA	ATC	AGC	AGA	TAC	AAC	TAT	TAC	CTG	336
Ala	Arg	Glu	Lys	Ala	Leu	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Leu	
			100					105					110			
GAC	GTC	TGG	GGC	AAG	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA				375
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
		115					120					125				

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5					10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Ser	Tyr	
			20					25					30			
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val	
	50					55					60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Met	Val	Tyr	
	65				70					75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
									90					95		

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
100 105 110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmund Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA LIBRARY, LD2
 - (B) CLONE: LD2-1
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 22
 - (B) MAP POSITION: q11
 - (C) UNITS: Chromosome band number
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..333
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
- (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION:join(61..99, 145..165, 262..294)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GTG	GTG	ACT	CAG	CCA	CCC	TCA	GCG	TCT	GGG	ACC	CCC	GGA	CAG	AGG	GTC	48
Val	Val	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly	Thr	Pro	Gly	Gln	Arg	Val	
1				5				10						15		
ACC	ATC	TCT	TGT	TCT	GGA	AGC	AAC	TCC	ATC	CTT	GGA	AGT	AAG	TAT	GTA	96
Thr	Ile	Ser	Cys	Ser	Gly	Ser	Asn	Ser	Ile	Leu	Gly	Ser	Lys	Tyr	Val	
			20					25					30			
TAC	TGG	TAC	CAG	AAA	CTC	CCA	GGA	ACG	GCC	CCC	AAA	CTC	CTC	ATC	TAT	144
Tyr	Trp	Tyr	Gln	Lys	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	
		35					40					45				
AAG	AAT	GAT	CAG	CGG	CCC	TCA	GGG	GTC	TCT	GAC	CGA	TTC	TCT	GGC	TCC	192
Lys	Asn	Asp	Gln	Arg	Pro	Ser	Gly	Val	Ser	Asp	Arg	Phe	Ser	Gly	Ser	

50

55

60

AAG	TCT	GGC	ACC	TCG	GCC	TCC	CTG	GCC	ATC	AGT	GGG	CTC	CGG	TCC	GAG	240
Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Ser	Gly	Leu	Arg	Ser	Glu	
65					70					75					80	
GAT	GAG	GCT	GAC	TAT	TAC	TGT	GCA	CCA	TGG	GAT	GCC	AAC	CTG	GGT	GGC	288
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Pro	Trp	Asp	Ala	Asn	Leu	Gly	Gly	
				85					90					95		
CCG	GTG	TTC	GGC	GGA	GGG	ACC	AAG	CTG	ACC	GTC	CTA	AGT	CAG	CCC		333
Pro	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Ser	Gln	Pro		
			100					105					110			

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val	Val	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly	Thr	Pro	Gly	Gln	Arg	Val	
1				5					10					15		
Thr	Ile	Ser	Cys	Ser	Gly	Ser	Asn	Ser	Ile	Leu	Gly	Ser	Lys	Tyr	Val	
			20					25					30			
Tyr	Trp	Tyr	Gln	Lys	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	
			35				40					45				
Lys	Asn	Asp	Gln	Arg	Pro	Ser	Gly	Val	Ser	Asp	Arg	Phe	Ser	Gly	Ser	
	50					55					60					
Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Ser	Gly	Leu	Arg	Ser	Glu	
	65				70					75					80	
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Pro	Trp	Asp	Ala	Asn	Leu	Gly	Gly	
				85					90					95		
Pro	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Ser	Gln	Pro		
			100					105					110			

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapiens

- (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA Library, LD2
- (B) CLONE: LD2-4

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..375
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly	
1 5 10 15	
TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT	96
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser	
20 25 30	
GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG	192
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val	
50 55 60	
AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT	288
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG	336
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met	
100 105 110	
GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA	375
Asp Val Trp Gly Lys Gly Thr Val Thr Val Ser Ser	
115 120 125	

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
20 25 30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-4

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..312

(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3

(B) LOCATION:join(64..96, 142..162, 259..282)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTA	GGA	GAC	AGA		48
Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg		
1			5					10					15			
ATC	ACT	TGC	CGG	ACA	AGT	CAG	ACC	ATT	AGC	AGA	AAT	TTA	AAT			96
Thr	Ile	Thr	Cys	Arg	Thr	Ser	Gln	Thr	Ile	Ser	Arg	Asn	Leu	Asn		
	20						25					30				
TAT	CAG	CAG	AAA	CCA	GGG	AAA	GCC	CCT	AAG	CTC	CTG	ATC	TAT	GCT		144
Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala		
	35					40					45					
TCC	AGT	TTG	CAA	AGT	GGG	GTC	CCA	TCA	AGG	TTC	AGT	GGC	AGT	GGA		192
Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly		
	50				55					60						
GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AAT	AGT	CTA	CAA	CCT	GAA	GAT		240
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Ser	Leu	Gln	Pro	Glu	Asp		
				70				75						80		
GCA	ACT	TAC	TAC	TGT	CAA	CAG	AGT	TAC	ACT	ACC	CCT	TCG	TTC	GGC		288
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Thr	Thr	Pro	Ser	Phe	Gly		
			85					90					95			
CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA									312
Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys									
			100													

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5					10					15		
Val	Thr	Ile	Thr	Cys	Arg	Thr	Ser	Gln	Thr	Ile	Ser	Arg	Asn	Leu	Asn	
		20						25					30			
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				
Thr	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	
		50				55					60					
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Ser	Leu	Gln	Pro	Glu	Asp	
		65			70				75					80		
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Thr	Thr	Pro	Ser	Phe	Gly	

Gln Gly Thr Lys Val Glu Ile Lys
100

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-4

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CAG	GTG	AAA	CTG	CTC	GAG	TCT	GGG	GGA	GGC	TTG	GTC	CAG	CCG	GGG	GGG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
1				5				10						15		
TCC	CTG	AGA	CTC	TCC	TGT	GTA	GCG	TCT	GGA	TTC	ACC	TTC	AGG	AGT	TAT	96
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Ser	Tyr	
			20					25					30			
GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGC	CTG	GAG	TGG	GTG	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
GCT	TTT	ATA	TGG	TTT	GAT	GGA	AGT	AAT	AAA	GGA	TAT	GTA	GAC	TCC	GTG	192
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val	
		50				55					60					

AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG CTC TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr	
65 70 75 80	
CTG CAA ATG AAT AGC CTG AGA GCC GAG GAC ACG GCT GTA TAT TAT TGT	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC AAC TAT TAC CTG	336
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu	
100 105 110	
GAC GTC TGG GGC AAG GGG GCC ACG GTC ACC GTC TCC TCA	375
Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser	
115 120 125	

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr	
20 25 30	
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val	
50 55 60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr	
65 70 75 80	
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu	
100 105 110	
Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser	
115 120 125	

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 (D) DEVELOPMENTAL STAGE: adult
 (E) HAPLOTYPE: diploid
 (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDND library. LD2
 (B) CLONE: LD2-5
- (viii) POSITION IN GENOME:
 (A) CHROMOSOME/SEGMENT: chromosome 2
 (B) MAP POSITION: p11
 (C) UNITS: Chromosome band number
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..318
 (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
- (ix) FEATURE:
 (A) NAME/KEY: CDR1, CDR2, CDR3
 (B) LOCATION: join(64..96, 142..162, 259..288)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GTG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	ATA	GGC	GAC	AGA		48
Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Ile	Gly	Asp	Arg		
1				5					10					15			
GTC	ACC	ATC	ACT	TGC	CGG	GCA	AGT	CAG	AGC	GTT	ACC	AGG	TCT	TTA	AAT		96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Val	Thr	Arg	Ser	Leu	Asn		
			20					25					30				
TGG	TAT	CAG	CAG	AAA	CCA	GGG	AAA	GCC	CCT	AGG	CTC	CTA	ATC	TTT	GCT		144
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Arg	Leu	Leu	Ile	Phe	Ala		
			35				40					45					
GCG	TCC	ACT	TTG	CAA	AGT	GGG	GTC	CCA	TCA	AGG	TTC	AGT	GGC	AGT	GGA		192
Ala	Ser	Thr	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly		
			50			55					60						
TCT	GGG	ACA	GAT	TTC	ACC	CTC	ACC	ATC	AGC	AGT	CTG	CAA	CCT	GAG	GAT		240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp		
			65		70				75					80			
TTT	GGA	ACT	TAC	TAC	TGT	CAA	CAG	AAT	TAC	AGG	ACC	CCT	CAG	TGG	ACG		288
Phe	Gly	Thr	Tyr	Tyr	Cys	Gln	Gln	Asn	Tyr	Arg	Thr	Pro	Gln	Trp	Thr		
				85				90						95			
TTC	GGC	CAA	GGG	ACC	AAG	GTA	GAA	ATC	AAA								318
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys								
			100					105									

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid

28
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
1 5 10 15
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn
20 25 30
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala
35 40 45
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80
Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr
85 90 95
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-10

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3
(B) LOCATION: join(91..105, 148..198, 298..345)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CAG	GTG	AAA	CTG	CTC	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCG	GGG	GGG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5				10						15		
TCC	CTG	AGA	CTC	TCC	TGT	GTA	GCG	TCT	GGA	TTC	ACC	CTC	AGG	AGT	TAT	96
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Ser	Tyr	
			20					25					30			
GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGC	CTG	GAG	TGG	GTG	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
GCT	TTT	ATA	TGG	TTT	GAT	GGA	AGT	AAT	AAA	GGA	TAT	GTA	GAC	TCC	GTG	192
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val	
	50					55					60					
AAG	GGC	CGA	TTC	ACC	ATC	TCC	CGA	GAC	AAT	TCC	AAG	AAC	ATG	GTC	TAT	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Met	Val	Tyr	
				175					180					185		
CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCC	GAT	GAC	ACG	GCT	GTA	TAT	TAT	TAT	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Tyr	
				85					90					95		
TGT	GCG	AGA	GAG	AAG	GCG	CTT	CGG	GGA	ATC	AGC	AGA	TAC	AAC	TAT	TAC	336
Cys	Ala	Arg	Glu	Lys	Ala	Leu	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	
			100					105					110			
CTG	GAC	GTC	TGG	GGC	AAG	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA			378
Leu	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser			
		115					120					125				

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5					10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Ser	Tyr	
			20					25					30			
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val	
	50					55					60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Met	Val	Tyr	
	65				70				75					80		

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Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr
      85                      90                      95

Lys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr
      100                    105                    110

Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
      115                    120                    125

```

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD2
 - (B) CLONE: LD2-10
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 22
 - (B) MAP POSITION: q11
 - (C) UNITS: Chromosome band number
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..333
 - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
- (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(61..102, 148..168, 265..294)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GTG GTG ACT CAG GAG CCC TCA CTG ACT GTG TCC CCA GGA GGG ACA GTC	48
Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val	
1 5 10 15	
ACT CTC ACC TGT GCT TCC AGC ACT GGG GCA GTC ACC AGG GGT TAC TAT	96
Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr	
20 25 30	
CCA AAC TGG TTC CAG CAG AAG CCT GGA CAA GCA CCC AGG GCA CTG ATT	144
Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile	
35 40 45	

TAT	AGT	ACA	AAC	AAA	AAA	CAC	TCC	TGG	ACC	CCT	GCC	CGG	TTC	TCA	GGC	192
Tyr	Ser	Thr	Asn	Lys	Lys	His	Ser	Trp	Thr	Pro	Ala	Arg	Phe	Ser	Gly	
	50					55					60					
TCC	CTC	CTT	GGG	GGC	AAA	GCT	GCC	CTG	ACA	CTG	TCA	GGT	GTG	CAG	CCT	240
Ser	Leu	Leu	Gly	Gly	Lys	Ala	Ala	Leu	Thr	Leu	Ser	Gly	Val	Gln	Pro	
	65				70					75					80	
GAA	GAC	GAG	GCT	GAA	TAT	TAC	TGC	CTG	CTC	TAC	TAT	GGT	GGT	GCT	CAA	288
Glu	Asp	Glu	Ala	Glu	Tyr	Tyr	Cys	Leu	Leu	Tyr	Tyr	Gly	Gly	Ala	Gln	
				85					90					95		
CTC	GTA	TTC	GGC	GGA	GGG	ACC	AAG	CTG	ACC	GTC	CTA	CGT	CAG	CCC		333
Leu	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Arg	Gln	Pro		
			100					105					110			

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Val	Val	Thr	Gln	Glu	Pro	Ser	Leu	Thr	Val	Ser	Pro	Gly	Gly	Thr	Val	
1				5					10					15		
Thr	Leu	Thr	Cys	Ala	Ser	Ser	Thr	Gly	Ala	Val	Thr	Arg	Gly	Tyr	Tyr	
			20					25					30			
Pro	Asn	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Ala	Leu	Ile	
	35						40					45				
Tyr	Ser	Thr	Asn	Lys	Lys	His	Ser	Trp	Thr	Pro	Ala	Arg	Phe	Ser	Gly	
	50					55					60					
Ser	Leu	Leu	Gly	Gly	Lys	Ala	Ala	Leu	Thr	Leu	Ser	Gly	Val	Gln	Pro	
	65				70					75					80	
Glu	Asp	Glu	Ala	Glu	Tyr	Tyr	Cys	Leu	Leu	Tyr	Tyr	Gly	Gly	Ala	Gln	
				85					90					95		
Leu	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Arg	Gln	Pro		
			100					105					110			

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-11

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly	
1 5 10 15	
TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT	96
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser	
20 25 30	
GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG	192
Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val	
50 55 60	
AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT	288
Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG	336
Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met	
100 105 110	
GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA	375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: lymphocyte

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-11

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..315

(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3

(B) LOCATION:join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GTG	TTG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	ATA	CGA	GAC	AGA	48
Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Ile	Arg	Asp	Arg	
1				5				10						15		
GTC	ACC	ATC	ACT	TGC	CGG	GCA	AGT	CAG	AAC	ATT	GGC	AGT	TAT	TTA	AAT	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Gly	Ser	Tyr	Leu	Asn	
			20					25					30			
TGG	TAT	CAG	CAC	AAA	CCA	GGG	ACA	GCC	CCT	AAA	CTC	CTG	ATC	TAT	GCT	144
Trp	Tyr	Gln	His	Lys	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				
GTA	TCC	GCT	TTG	CAA	AGT	GGG	GTC	CCA	TCG	AGG	TTC	AGT	GGC	AGT	AGA	192
Val	Ser	Ala	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Arg	
	50					55				60						
TCT	GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGT	CTG	CAA	CCT	GAA	GAT	240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
65					70				75					80		
TTT	GCA	ACT	TAC	TAC	TGT	CAA	CAG	AGT	TAC	AGT	CCC	CCG	TAC	ACT	TTC	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Pro	Pro	Tyr	Thr	Phe	
			85					90						95		
GGC	CAG	GGG	ACC	AAC	CTG	CAG	ATC	AAA								315
Gly	Gln	Gly	Thr	Asn	Leu	Gln	Ile	Lys								
		100						105								

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Ile	Arg	Asp	Arg	
1				5				10						15		
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Gly	Ser	Tyr	Leu	Asn	
		20						25					30			
Trp	Tyr	Gln	His	Lys	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				
Val	Ser	Ala	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Arg	
	50					55				60						
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe
 85 90 95

Gly Gln Gly Thr Asn Leu Gln Ile Lys
 100 105

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-14

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CAG	GTG	AAA	CTG	CTC	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCG	GGG	GGG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5					10					15		
TCC	CTG	AGA	GTC	GCC	TGT	GTA	GCG	TCT	GGA	TTC	ACC	TTC	AGG	AAT	TTT	96
Ser	Leu	Arg	Val	Ala	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Asn	Phe	
			20					25					30			
GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
			35				40					45				
GCT	TTT	ATT	TGG	TTT	GAT	GCA	AGT	AAT	AAA	GGA	TAT	GGA	GAC	TCC	GTT	192

Ala	Phe	Ile	Trp	Phe	Asp	Ala	Ser	Asn	Lys	Gly	Tyr	Gly	Asp	Ser	Val		
	50					55					60						
AAG	GGC	CGA	TTC	ACC	GTC	TCC	AGA	GAC	AAT	TCC	AAG	AAC	ACG	CTC	TAT	240	
Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	80	
65					70					75							
CTG	CAA	ATG	AAC	GGC	CTG	AGA	GCC	GAA	GAC	ACG	GCT	GTA	TAT	TAT	TGT	288	
Leu	Gln	Met	Asn	Gly	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	95	
				85					90								
GCG	AGA	GAG	AAG	GCG	GTT	CGG	GGA	ATT	AGT	AGA	TAC	AAC	TAC	TAC	ATG	336	
Ala	Arg	Glu	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	110	
			100					105									
GAC	GTC	TGG	GGC	AAG	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA				375	
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				125	
		115					120										

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly		
1				5					10					15			
Ser	Leu	Arg	Val	Ala	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Asn	Phe		
			20					25					30				
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
		35				40						45					
Ala	Phe	Ile	Trp	Phe	Asp	Ala	Ser	Asn	Lys	Gly	Tyr	Gly	Asp	Ser	Val		
	50					55					60						
Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr		
65					70					75				80			
Leu	Gln	Met	Asn	Gly	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
				85					90					95			
Ala	Arg	Glu	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met		
		100						105					110				
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser					
		115					120					125					

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: lymphocyte
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD2
 - (B) CLONE: LD2-14
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: Chromosome band number
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..315
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
- (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION:join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GTG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTG	GGA	GAC	AGA	48
Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5				10						15		
GTC	ACC	ATC	ACT	TGC	CGG	GCA	AGT	CAG	AGC	ATT	ATC	AAC	AAT	TTA	AAT	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ile	Asn	Asn	Leu	Asn	
			20					25					30			
TGG	TAT	CAG	CAG	AAA	CCA	GGC	AAA	GCC	CCT	GAA	CTC	CTG	ATC	TAT	GCT	144
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Glu	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				
GCA	TCC	AGT	TTG	CAA	AGT	GGG	GTC	CCT	TCA	AGG	TTC	CGT	GGC	AGT	GGA	192
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Arg	Gly	Ser	Gly	
	50					55					60					
TCT	GGG	AGA	GAT	TTC	ACT	CTC	ACC	GTC	ACC	AGT	CTG	CAA	CCT	GAA	GAT	240
Ser	Gly	Arg	Asp	Phe	Thr	Leu	Thr	Val	Thr	Ser	Leu	Gln	Pro	Glu	Asp	
65				70				75						80		
TTT	GCA	ACT	TAC	TAC	TGT	CAA	CAG	AGT	TAC	AGT	ACC	CTG	TGG	ACG	TTC	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Leu	Trp	Thr	Phe	
			85					90					95			
GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA								315
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys								
		100					105									

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1           5           10           15
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn
      20           25           30
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala
      35           40           45
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly
      50           55           60
Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp
      65           70           75           80
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe
      85           90           95
Gly Gln Gly Thr Lys Val Glu Ile Lys
      100           105

```

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library
- (B) CLONE: LD2-17

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.43
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION:1..375

(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3

(B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CAG	GTG	AAA	CTG	CTC	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCG	GGG	GGG		48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly		
1				5				10						15			
TCC	CTG	AGA	CTC	TCC	TGT	GTA	GCG	TCT	GGA	TTC	ACC	TTC	AGG	AGT	TAT		96
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Ser	Tyr		
			20					25					30				
GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGC	CTG	GAG	TGG	GTG		144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
		35					40					45					
GCT	TTT	ATA	TGG	TTT	GAT	GGA	AGT	AAT	AAA	GGA	TAT	GTA	GAC	TCC	GTG		192
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val		
	50					55					60						
AAG	GGC	CGA	TTC	ACC	ATC	TCC	CGA	GAC	AAT	TCC	AAG	AAC	ACG	CTC	TAT		240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr		
	65				70				75					80			
CTG	CAA	ATG	AAG	AGC	CTG	AGA	GCC	GAG	GAC	ACG	GCT	GTA	TAT	TAT	TGT		288
Leu	Gln	Met	Lys	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
				85				90						95			
GCG	AGA	GAG	AAG	GCG	CTT	CGG	GGA	ATC	AGT	AGA	TAC	AAC	TAT	TAC	CTG		336
Ala	Arg	Glu	Lys	Ala	Leu	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Leu		
			100				105						110				
GAC	GTC	TGG	GGC	AAG	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA					375
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser					
		115					120				125						

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5				10						15		
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Ser	Tyr	
			20					25					30			
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val	
	50					55					60					

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
100 105 110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-17

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTG ATG ACC CAG TCT CCA TTC TCC CTG TCT GCA TCT GTA GGA GAC AGA
Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT AGG AGT TTT TTA AGT
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser
20 25 30

48

96

TGG	TAT	CAG	CAG	AAA	CCA	GGG	ACA	GCC	CCT	AAG	CTC	CTG	ATC	TAT	GCT	144
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				
GCA	TCC	AGG	TTG	CAA	AGT	GGG	GTC	CCA	TCA	AGG	TTC	AGT	GGC	AGT	GGG	192
Ala	Ser	Arg	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	
		50				55					60					
TCT	GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	ACT	CTG	CAA	CCT	GAA	GAT	240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Thr	Leu	Gln	Pro	Glu	Asp	
		65			70					75					80	
TTT	GCG	ACT	TAC	TAC	TGT	CAA	CAG	AGT	TAC	AGT	GCC	CCT	TGG	ACG	TTC	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Ala	Pro	Trp	Thr	Phe	
				85				90						95		
GGC	CAA	GGG	ACC	AAG	CTG	GAA	ATC	AAA								315
Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys								
		100						105								

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Val	Met	Thr	Gln	Ser	Pro	Phe	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5					10					15		
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Arg	Ser	Phe	Leu	Ser	
			20					25					30			
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				
Ala	Ser	Arg	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	
		50				55					60					
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Thr	Leu	Gln	Pro	Glu	Asp	
		65			70					75					80	
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Ala	Pro	Trp	Thr	Phe	
				85					90					95		
Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys								
		100						105								

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library LD2
 - (B) CLONE: LD2-20
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 14
 - (B) MAP POSITION: q32.3
 - (C) UNITS: Chromosome band number
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..375
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
- (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CAG	GTG	AAA	CTG	CTC	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCG	GGG	GGG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5				10						15		
TCC	CTG	AGA	CTC	TCC	TGT	GTA	GCG	TCT	GGA	TTC	ACC	TCC	AGG	AGT	TAT	96
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Ser	Arg	Ser	Tyr	
			20					25						30		
GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGC	CTG	GAG	TGG	GTG	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
	50					55					60					
GCT	TTT	ATA	TGG	TTT	GAT	GGA	AGT	AAT	AAA	GGA	TAT	GTA	GAC	TCC	GTG	192
Ala	Phe	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Gly	Tyr	Val	Asp	Ser	Val	
65					70					75					80	
AAG	GGC	CGA	TTC	ACC	ATC	TCC	CGA	GAC	AAT	TCC	AAG	AAC	ACG	CTC	TAT	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
				85					90					95		
CTG	CAA	ATG	AAG	AGC	CTG	AGA	GCC	GAG	GAC	ACG	GCT	GTA	TAT	TAT	TGT	288
Leu	Gln	Met	Lys	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			100					105					110			
GCG	AGA	GAG	AAG	GCG	CTT	CGG	GGA	ATC	AGT	AGA	TAC	AAC	TAT	TAC	CTG	336
Ala	Arg	Glu	Lys	Ala	Leu	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Leu	
			205					210					215			
GAC	GTC	TGG	GGC	AAG	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA				375
Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser				
	115					120					125					

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1          5          10          15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr
      20          25          30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35          40          45
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
      50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
      65          70          75
Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
      85          90          95
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
      100          105          110
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
      115          120          125

```

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD2
- (B) CLONE: LD2-20

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 2
 (B) MAP POSITION: p11
 (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION:1..315
 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
 (B) LOCATION:join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

3TG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTA	GGA	GAC	AGA	48
Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5				10						15		
GTC	ACC	ATC	ACT	TGC	CGG	GCA	AGT	CAG	AGC	ATT	AGC	AGC	TAT	TTA	AAT	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn	
			20					25					30			
TGG	TAT	CAG	CAG	AAA	CCA	GGG	AAA	GCC	CCT	AAG	CTC	CTG	ATC	TAT	GCT	144
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				
GCA	TCC	AGT	TTG	CAA	AGT	GGG	GTC	CCA	TCA	AGG	TTC	AGT	GGC	AGT	GGA	192
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	
		50				55					60					
TCT	GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGT	CTG	CAA	CCT	GAA	GAT	240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
65				70					75					80		
TTT	GCA	ACT	TAC	TAC	TGT	CAA	CAG	AGT	TAC	AGT	ACC	CGA	TTC	ACT	TTC	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Thr	Arg	Phe	Thr	Phe	
			85					90						95		
GGC	CCT	GGG	ACC	AAA	GTG	GAT	ATC	AAA								315
Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys								
		100						105								

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5				10						15		
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	Leu	Asn	
			20					25					30			
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe
85 90 95
Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1
- (B) CLONE: LD1-6-17

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..384
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(91..105, 148..198, 295..351)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CAG GTG AAA CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	
TCC CTG AGA CTT TCC TGT GCA GCG TCT GGA TTT ACC TTC AGT AGC TAT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
20 25 30	

GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
GCA	GAT	ATA	TGG	TTT	GAT	GGA	GGT	AAT	AAA	CAT	TAT	GCA	GAC	TTC	GTG	192
Ala	Asp	Ile	Trp	Phe	Asp	Gly	Gly	Asn	Lys	His	Tyr	Ala	Asp	Phe	Val	
	50					55					60					
AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAT	TCC	AAG	AAC	ACG	GTG	TAT	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Val	Tyr	
	65				70				75						80	
CTA	CAA	ATG	AAC	AGC	CTG	AGA	GTC	GAG	GAC	ACG	GCT	GTG	TAT	TAC	TGT	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Val	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
GCG	AGG	GAT	TAC	TAT	AGC	GTT	ACT	AAG	AAA	CTC	AGA	CTC	CAC	TAC	TAC	336
Ala	Arg	Asp	Tyr	Tyr	Ser	Val	Thr	Lys	Lys	Leu	Arg	Leu	His	Tyr	Tyr	
			100					105					110			
TAC	TAC	ATG	GAC	GTC	TGG	GGC	AAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA	384
Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	
		220					225					230				

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1				5					10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	
			20					25					30			
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
Ala	Asp	Ile	Trp	Phe	Asp	Gly	Gly	Asn	Lys	His	Tyr	Ala	Asp	Phe	Val	
	50					55					60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Val	Tyr	
	65				70				75					80		
Leu	Gln	Met	Asn	Ser	Leu	Arg	Val	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
Ala	Arg	Asp	Tyr	Tyr	Ser	Val	Thr	Lys	Lys	Leu	Arg	Leu	His	Tyr	Tyr	
			100					105					110			
Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	
		115					120					125				

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1
- (B) CLONE: LD1-6-17

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 2
- (B) MAP POSITION: p11
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION: join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GTG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTA	GGA	GAC	AGA	48
Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5					10					15		
GTC	ACC	ATC	ACT	TGC	CGG	GCA	AGT	CAG	GGC	ATT	AGA	AAT	GAT	TTA	ACC	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Asp	Leu	Thr	
			20					25					30			
TGG	TAT	CAG	CAA	AAA	CCA	GGG	AAA	GCC	CCT	AAG	CTC	CTG	ATC	TAT	GCT	144
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				
GCA	TCC	AAT	TTA	CAA	AGT	GGG	GTC	CCA	TCA	AGG	TTC	AGC	GGC	AGT	GGA	192
Ala	Ser	Asn	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	
		50				55					60					
TCT	GGC	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGC	CTG	CAG	CCT	GAA	GAT	240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
		65			70				75					80		
TTT	GCA	ACT	TAT	TAC	TGT	CTA	CAA	GAT	AAC	AAT	TTC	CCG	TAC	ACT	TTT	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Asp	Asn	Asn	Phe	Pro	Tyr	Thr	Phe	
				85				90						95		

GGC CAG GGG ACC AAG CTG GAG ATC AAA
Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
35 40 45

Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe
85 90 95

Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS
- (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
(D) DEVELOPMENTAL STAGE: adult
(E) HAPLOTYPE: diploid
(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- IMMEDIATE SOURCE:
(A) LIBRARY: cDNA library, LD1 and LD2
(B) CLONE: LD1/2-6-3

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
 (B) MAP POSITION: q32.3
 (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION:1..375
 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
 (B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CAG	GTG	AAA	CTG	CTC	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCG	GGG	GGG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5				10						15		
TCC	CTG	AGA	GTC	GCC	TGT	GTA	GCG	TCT	GGA	TTC	ACC	TTC	AGG	AAT	TTT	96
Ser	Leu	Arg	Val	Ala	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Asn	Phe	
			20					25					30			
GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
GCT	TTT	ATT	TGG	TTT	GAT	GCA	AGT	AAT	AAA	GGA	TAT	GGA	GAC	TCC	GTT	192
Ala	Phe	Ile	Trp	Phe	Asp	Ala	Ser	Asn	Lys	Gly	Tyr	Gly	Asp	Ser	Val	
	50					55					60					
AAG	GGC	CGA	TTC	ACC	GTC	TCC	AGA	GAC	AAT	TCC	AAG	AAC	ACG	CTC	TAT	240
Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70					75					80	
CTG	CAA	ATG	AAC	GGC	CTG	AGA	GCC	GAA	GAC	ACG	GCT	GTA	TAT	TAT	TGT	288
Leu	Gln	Met	Asn	Gly	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90				95			
GCG	AGA	GAG	AAG	GCG	GTT	CGG	GGA	ATT	AGT	AGA	TAC	AAC	TAC	TAC	ATG	336
Ala	Arg	Glu	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	
			100					105					110			
GAC	GTC	TGG	GGC	AAG	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA				375
Asp	Val	Trp	Gly	Lys	Gly	Thr	Val	Val	Thr	Val	Ser	Ser				
		115					120					125				

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Gly	
1				5					10					15		
Ser	Leu	Arg	Val	Ala	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Asn	Phe	
			20					25					30			

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD1 and LD2
 - (B) CLONE: LD1/2-6-3
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: Chromosome band number
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..315
 - (D) OTHER INFORMATION: /product= "Immunoglobulin, Fab"
- (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(64..96, 142..162, 259..285)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

ATG	ATG	ACC	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTA	GGA	GAC	AGA	48
Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5					10					15		
ATC	ACC	ATC	ACT	TGC	CGG	GCA	AGT	CAG	AGC	ATT	ATC	AGA	TAT	TTA	AAT	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ile	Arg	Tyr	Leu	Asn	
			20					25					30			
TGG	TAT	CAG	CAC	AAA	CCA	GGG	AAA	GCC	CCT	AAG	CTC	CTG	ATC	CAT	ACT	144
Trp	Tyr	Gln	His	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	His	Thr	
		35					40					45				
ACA	TCC	AGT	TTG	CAA	AGT	GGG	GTC	CCG	TCA	AGG	TTC	AGT	GGC	AGT	GTA	192
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Val	
		50				55					60					
TCT	GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGT	CTG	CAA	CCT	GAA	GAT	240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
65				70					75					80		
TTT	GCA	ACT	TAC	TAC	TGT	CAA	CAG	AGT	TAC	ACT	ACC	CCG	TAC	ACT	TTT	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Thr	Thr	Pro	Tyr	Thr	Phe	
			85					90					95			
GGC	CAG	GGG	ACC	AAG	CTG	CAG	ATC	AAA								315
Gly	Gln	Gly	Thr	Lys	Leu	Gln	Ile	Lys								
			100					105								

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5					10					15		
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ile	Arg	Tyr	Leu	Asn	
		20						25					30			
Trp	Tyr	Gln	His	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	His	Thr	
		35					40					45				
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Val	
		50				55					60					
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
65				70					75					80		
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Thr	Thr	Pro	Tyr	Thr	Phe	
			85					90					95			
Gly	Gln	Gly	Thr	Lys	Leu	Gln	Ile	Lys								
			100					105								

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Rhesud D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid
- (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1 and LD2
- (B) CLONE: LD1/2-2-33

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: chromosome 14
- (B) MAP POSITION: q32.3
- (C) UNITS: Chromosome band number

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..375
- (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

- (A) NAME/KEY: CDR1, CDR2, CDR3
- (B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG	48
3ln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly	
1 5 10 15	
PCC CTG AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT	96
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe	
20 25 30	
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
GCT TTT ATT TGG TTT GAT GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT	192
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val	
50 55 60	
AAG GGC CGA TTC ACC GTC TCC AGA GAC AAT TCC AAG AAC ACG CTC TAT	240
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC ACG GCT GTA TAT TAT TGT	288
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

CGC AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC AAC TAC TAC ATG 336
 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

AAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

P1n Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: hyperimmune Resus D donor
- (D) DEVELOPMENTAL STAGE: adult
- (E) HAPLOTYPE: diploid

(G) CELL TYPE: Peripheral lymphocyte B

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD1 and LD2
 - (B) CLONE: LD1/2-6-33

- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: Chromosome band number

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..315
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

- (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION:join(64..96, 142..162, 259..285)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ATG	ATG	ACC	CAG	TCT	CCA	TCC	TTC	CTG	TCT	GCA	TCT	GTA	GGA	GAC	AGA	48
Val	Met	Thr	Gln	Ser	Pro	Ser	Phe	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5				10						15		
ATC	ACC	ATC	ACT	TGC	CGG	GCA	AGT	CAG	AGC	ATT	ATC	AGA	TAT	TTA	AAT	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ile	Arg	Tyr	Leu	Asn	
			20					25					30			
GGG	TAT	CAG	CAC	AAA	CCA	GGG	AAA	GCC	CCT	AAG	CTC	CTG	ATC	CAT	GCT	144
Trp	Tyr	Gln	His	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	His	Ala	
		35				40					45					
ACA	TCC	AGT	TTG	CAA	AGT	GGG	GTC	CCG	TCA	AGG	TTC	AGT	GGC	AGT	GTA	192
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Val	
		50				55					60					
CTT	GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGT	CTG	CAA	CCT	GAA	GAT	240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
					70				75					80		
TTT	GCA	ACT	TAC	TAC	TGT	CAA	CAG	AGT	TAC	ACT	ACC	CCG	TAC	ACT	TTT	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Thr	Thr	Pro	Tyr	Thr	Phe	
				85				90						95		
GGC	CAG	GGG	ACC	AAG	CTG	CAG	ATC	AAA								315
Gly	Gln	Gly	Thr	Lys	Leu	Gln	Ile	Lys								
			100					105								

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Val	Met	Thr	Gln	Ser	Pro	Ser	Phe	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg
1				5				10						15	

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe
85 90 95

Gly Gln Gly Thr Lys Leu Gln Ile Lys
100 105